



OIKE

RAW SEQUENCE LISTING

DATE: 01/24/2002

PATENT APPLICATION: US/09/983,025

TIME: 14:48:34

Input Set : A:\OXVIG1A.txt

Output Set: N:\CRF3\01242002\I983025.raw

PS

ENTERED

3 <110> APPLICANT: OXVIG, Claus
 4 OVERGAARD, Michael T.
 6 <120> TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
 8 <130> FILE REFERENCE: OXVIG=1A
 10 <140> CURRENT APPLICATION NUMBER: US 09/983,025
 11 <141> CURRENT FILING DATE: 2001-10-22
 13 <150> PRIOR APPLICATION NUMBER: US 60/241,840
 14 <151> PRIOR FILING DATE: 2000-10-20
 16 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01571
 17 <151> PRIOR FILING DATE: 2000-10-20
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 8527
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(5373)
 31 <223> OTHER INFORMATION: prepro-PAPP-A2 coding sequence
 34 <220> FEATURE:
 35 <221> NAME/KEY: 3'UTR
 36 <222> LOCATION: (5377)..(8527)
 37 <223> OTHER INFORMATION:
 40 <220> FEATURE:
 41 <221> NAME/KEY: mat_peptide
 42 <222> LOCATION: (700)..()
 43 <223> OTHER INFORMATION:
 46 <220> FEATURE:
 47 <221> NAME/KEY: sig_peptide
 48 <222> LOCATION: (1)..(66)
 49 <223> OTHER INFORMATION:
 52 <220> FEATURE:
 53 <221> NAME/KEY: misc_feature
 54 <222> LOCATION: (1)..(66)
 55 <223> OTHER INFORMATION: prepro part of PAPP-A2
 58 <220> FEATURE:
 59 <221> NAME/KEY: misc_feature
 60 <222> LOCATION: (67)..(699)
 61 <223> OTHER INFORMATION: pro part of PAPP-A2
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 66 Met Met Cys Leu Lys Ile Leu Arg Ile Ser Leu Ala Ile Leu Ala

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Input Set : A:\OXVIG1A.txt
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Line	Sequence	Score
67	-230	
69	ggg tgg gca ctc	-225
70	Gly Trp Ala Leu	-210
71	-215	
73	aag aaa tcc ttg	-195
74	Lys Lys Ser Leu	-200
75	-200	
77	gaa gga gaa cgt	-185
78	Glu Gly Glu Arg	-180
79	-185	
81	gct tct cca cag	-170
82	Ala Ser Pro Gln	-165
83	-170	
85	ggg aac tac cta	-155
86	Gly Asn Tyr Leu	-150
87	-155	
89	cat aca gga cgc	-140
90	His Thr Gly Arg	-135
91	-140	
93	ctt gtt ccc cca	-125
94	Leu Val Pro Pro	-120
95	-125	
97	gca gtt gaa gag	-110
98	Ala Val Glu Glu	-105
99	-110	
101	ggg caa tct gag	-95
102	Gly Gln Ser Glu	-90
103	-95	
105	aga tcc aag gag	-75
106	Arg Ser Lys Glu	-80
107	-80	
109	atg gct gcc act	-60
110	Met Ala Ala Thr	-65
111	-65	
113	aaa cca gag acc	-45
114	Lys Pro Glu Thr	-40
115	-50	
117	caa gtg tgg aag	-30
118	Gln Val Trp Lys	-25
119	-30	
121	tct tca cat ttc	-15
122	Ser Ser His Phe	-10
123	-15	
125	aaa aag agt cca	5
126	Lys Lys Ser Pro	10
127	-1	
129	tac cga gaa gca	25
130	Tyr Arg Glu Ala	30
131	15	

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133 tac ttc tct ggg agg cgg gag cgg ctg ctg ctg cgt cca gaa gtg ctg 837
 134 Tyr Phe Ser Gly Arg Arg Glu Arg Leu Leu Leu Arg Pro Glu Val Leu 45
 135 35 40 885
 137 gct gag att ccc cgg gag gcg ttc aca gtg gaa gcc tgg gtt aaa ccg 60
 138 Ala Glu Ile Pro Arg Glu Ala Phe Thr Val Glu Ala Trp Val Lys Pro 60 933
 139 50 55 75 981
 141 gag gga gga cag aac aac cca gcc atc atc gca ggt gtg ttt gat aac 75
 142 Glu Gly Gly Gln Asn Asn Pro Ala Ile Ile Ala Gly Val Phe Asp Asn 70
 143 65 70 90 1029
 145 tgc tcc cac act gtc agt gac aaa ggc tgg gcc ctg ggg atc cgc tca 90
 146 Cys Ser His Thr Val Ser Asp Lys Gly Trp Ala Leu Gly Ile Arg Ser 85
 147 80 105 110 1077
 149 ggg aag gac aag gga aag cgg gat gct cgc ttc ttc ttc tcc ctg tgc 105
 150 Gly Lys Asp Lys Gly Lys Arg Asp Ala Arg Phe Phe Phe Ser Leu Cys 100
 151 95 100 125 1125
 153 acc gac cgc gtg aag aaa gcc acc atc ttg att agc cac agt cgc tac 120
 154 Thr Asp Arg Val Lys Lys Ala Thr Ile Leu Ile Ser His Ser Arg Tyr 115
 155 115 120 140 1173
 157 caa cca ggc aca tgg acc cat gtg gca gcc act tac gat gga cgg cac 135
 158 Gln Pro Gly Thr Trp Thr His Val Ala Ala Thr Tyr Asp Gly Arg His 130
 159 130 155 1221
 161 atg gcc ctg tat gtg gat ggc act cag gtg gct agc agt cta gac cag 150
 162 Met Ala Leu Tyr Val Asp Gly Thr Gln Val Ala Ser Ser Leu Asp Gln 145
 163 145 170 1269
 165 tct ggt ccc ctg aac agc ccc ttc atg gca tct tgc cgc tct ttg ctg 165
 166 Ser Gly Pro Leu Asn Ser Pro Phe Met Ala Ser Cys Arg Ser Leu Leu 160
 167 160 185 1317
 169 ctg ggg gga gac agc tct gag gat ggg cac tat ttc cgt gga cac ctg 180
 170 Leu Gly Gly Asp Ser Ser Glu Asp Gly His Tyr Phe Arg Gly His Leu 175
 171 175 180 205 1365
 173 ggc aca ctg gtt ttc tgg tgg acc gcc ctg cca caa agc cat ttt cag 195
 174 Gly Thr Leu Val Phe Trp Ser Thr Ala Leu Pro Gln Ser His Phe Gln 200
 175 195 220 1413
 177 cac agt tct cag cat tca agt ggg gag gag gaa gcg act gac ttg gtc 215
 178 His Ser Ser Gln His Ser Ser Gly Glu Glu Glu Ala Thr Asp Leu Val 210
 179 210 235 1461
 181 ctg aca gcg agc ttt gag cct gtg aac aca gag tgg gtt ccc ttt aga 225
 182 Leu Thr Ala Ser Phe Glu Pro Val Asn Thr Glu Trp Val Pro Phe Arg 230
 183 225 250 1509
 185 gat gag aag tac cca cga ctt gag gtt ctg cag ggc ttt gag cca gag 245
 186 Asp Glu Lys Tyr Pro Arg Leu Glu Val Leu Gln Gly Phe Glu Pro Glu 240
 187 240 265 1557
 189 cct gag att ctg tgg cct ttg cag ccc cca ctg tgt ggg caa aca gtc 260
 190 Pro Glu Ile Leu Ser Pro Leu Gln Pro Pro Leu Cys Gly Gln Thr Val 255
 191 255 280 1605
 193 tgt gac aat gtg gaa ttg atc tcc cag tac aat gga tac tgg ccc ctt 275
 194 Cys Asp Asn Val Glu Leu Ile Ser Gln Tyr Asn Gly Tyr Trp Pro Leu 280
 195 275 285
 197 cgg gga gag aag gtg ata cgc tac cag gtg gtg aac atc tgt gat gat

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198	Arg	Gly	Glu	Lys	Val	Ile	Arg	Tyr	Gln	Val	Val	Asn	Ile	Cys	Asp	Asp	
199				290					295					300			
201	gag	ggc	cta	aac	ccc	att	gtg	agt	gag	gag	cag	att	cgt	ctg	cag	cac	1653
202	Glu	Gly	Leu	Asn	Pro	Ile	Val	Ser	Glu	Glu	Gln	Ile	Arg	Leu	Gln	His	
203				305					310					315			
205	gag	gca	ctg	aat	gag	gcc	ttc	agc	cgc	tac	aac	atc	agc	tgg	cag	ctg	1701
206	Glu	Ala	Leu	Asn	Glu	Ala	Phe	Ser	Arg	Tyr	Asn	Ile	Ser	Trp	Gln	Leu	
207				320					325					330			
209	agc	gtc	cac	cag	gtc	cac	aat	tcc	acc	ctg	cga	cac	cgg	gtt	gtg	ctt	1749
210	Ser	Val	His	Gln	Val	His	Asn	Ser	Thr	Leu	Arg	His	Arg	Val	Val	Leu	
211	335						340					345				350	
213	gtg	aac	tgt	gag	ccc	agc	aag	att	ggc	aat	gac	cat	tgt	gac	ccc	gag	1797
214	Val	Asn	Cys	Glu	Pro	Ser	Lys	Ile	Gly	Asn	Asp	His	Cys	Asp	Pro	Glu	
215							355							360		365	
217	tgt	gag	cac	cca	ctc	aca	ggc	tat	gat	ggg	ggt	gac	tgc	cgc	ctg	cag	1845
218	Cys	Glu	His	Pro	Leu	Thr	Gly	Tyr	Asp	Gly	Gly	Asp	Cys	Arg	Leu	Gln	
219				370					375					380			
221	ggc	cgc	tgc	tac	tcc	tgg	aac	cgc	agg	gat	ggg	ctc	tgt	cac	gtg	gag	1893
222	Gly	Arg	Cys	Tyr	Ser	Trp	Asn	Arg	Arg	Asp	Gly	Leu	Cys	His	Val	Glu	
223				385					390					395			
225	tgt	aac	aac	atg	ctg	aac	gac	ttt	gac	gac	gga	gac	tgc	tgc	gac	ccc	1941
226	Cys	Asn	Asn	Met	Leu	Asn	Asp	Phe	Asp	Asp	Gly	Asp	Cys	Cys	Asp	Pro	
227				400				405					410				
229	cag	gtg	gct	gat	gtg	cgc	aag	acc	tgc	ttt	gac	cct	gac	tca	ccc	aag	1989
230	Gln	Val	Ala	Asp	Val	Arg	Lys	Thr	Cys	Phe	Asp	Pro	Asp	Ser	Pro	Lys	
231	415						420					425				430	
233	agg	gca	tac	atg	agt	gtg	aag	gag	ctg	aag	gag	gcc	ctg	cag	ctg	aac	2037
234	Arg	Ala	Tyr	Met	Ser	Val	Lys	Glu	Leu	Lys	Glu	Ala	Leu	Gln	Leu	Asn	
235							435				440				445		
237	agt	act	cac	ttc	ctc	aac	atc	tac	ttt	gcc	agc	tca	gtg	cgg	gaa	gac	2085
238	Ser	Thr	His	Phe	Leu	Asn	Ile	Tyr	Phe	Ala	Ser	Ser	Val	Arg	Glu	Asp	
239				450					455					460			
241	ctt	gca	ggt	gct	gcc	acc	tgg	cct	tgg	gac	aag	gac	gct	gtc	act	cac	2133
242	Leu	Ala	Gly	Ala	Ala	Thr	Trp	Pro	Trp	Asp	Lys	Asp	Ala	Val	Thr	His	
243				465					470					475			
245	ctg	ggt	ggc	att	gtc	ctc	agc	cca	gca	tat	tat	ggg	atg	cct	ggc	cac	2181
246	Leu	Gly	Gly	Ile	Val	Leu	Ser	Pro	Ala	Tyr	Tyr	Gly	Met	Pro	Gly	His	
247				480				485					490				
249	acc	gac	acc	atg	atc	cat	gaa	gtg	gga	cat	gtt	ctg	gga	ctc	tac	cat	2229
250	Thr	Asp	Thr	Met	Ile	His	Glu	Val	Gly	His	Val	Leu	Gly	Leu	Tyr	His	
251	495						500					505			510		
253	gtc	ttt	aaa	gga	gtc	agt	gaa	aga	gaa	tcc	tgc	aat	gac	ccc	tgc	aag	2277
254	Val	Phe	Lys	Gly	Val	Ser	Glu	Arg	Glu	Ser	Cys	Asn	Asp	Pro	Cys	Lys	
255							515					520			525		
257	gag	aca	gtg	cca	tcc	atg	gaa	acg	gga	gac	ctc	tgt	gcc	gac	acc	gcc	2325
258	Glu	Thr	Val	Pro	Ser	Met	Glu	Thr	Gly	Asp	Leu	Cys	Ala	Asp	Thr	Ala	
259							530							540			
261	ccc	act	ccc	aag	agt	gag	ctg	tgc	cgg	gaa	cca	gag	ccc	act	agt	gac	2373
262	Pro	Thr	Pro	Lys	Ser	Glu	Leu	Cys	Arg	Glu	Pro	Glu	Pro	Thr	Ser	Asp	

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263	545	550	555	
265	acc tgt ggc ttc act cgc ttc cca ggg gct ccg ttc acc aac tac atg	2421		
266	Thr Cys Gly Phe Thr Arg Phe Pro Gly Ala Pro Phe Thr Asn Tyr Met			
267	560 565 570			
269	agc tac acg gat gat aac tgc act gac aac ttc act cct aac caa gtg	2469		
270	Ser Tyr Thr Asp Asp Asn Cys Thr Asp Asn Phe Thr Pro Asn Gln Val			
271	575 580 585 590			
273	gcc cga atg cat tgc tat ttg gac cta gtc tat cag cag tgg act gaa	2517		
274	Ala Arg Met His Cys Tyr Leu Asp Leu Val Tyr Gln Gln Trp Thr Glu			
275	595 600 605			
277	agc aga aag ccc acc ccc atc ccc att cca cct atg gtc atc gga cag	2565		
278	Ser Arg Lys Pro Thr Pro Ile Pro Ile Pro Pro Met Val Ile Gly Gln			
279	610 615 620			
281	acc aac aag tcc ctc act atc cac tgg ctg cct cct att agt gga gtt	2613		
282	Thr Asn Lys Ser Leu Thr Ile His Trp Leu Pro Pro Ile Ser Gly Val			
283	625 630 635			
285	gta tat gac agg gcc tca ggc agc ttg tgt ggc gct tgc act gaa gat	2661		
286	Val Tyr Asp Arg Ala Ser Gly Ser Leu Cys Gly Ala Cys Thr Glu Asp			
287	640 645 650			
289	ggg acc ttt cgt cag tat gtg cac aca gct tcc tcc cgg cgg gtg tgt	2709		
290	Gly Thr Phe Arg Gln Tyr Val His Thr Ala Ser Ser Arg Arg Val Cys			
291	655 660 665 670			
293	gac tcc tca ggt tat tgg acc cca gag gag gct gtg ggg cct cct gat	2757		
294	Asp Ser Ser Gly Tyr Trp Thr Pro Glu Glu Ala Val Gly Pro Pro Asp			
295	675 680 685			
297	gtg gat cag ccc tgc gag cca agc tta cag gcc tgg agc cct gag gtc	2805		
298	Val Asp Gln Pro Cys Glu Pro Ser Leu Gln Ala Trp Ser Pro Glu Val			
299	690 695 700			
301	cac ctg tac cac atg aac atg acg gtc ccc tgc ccc aca gaa ggc tgt	2853		
302	His Leu Tyr His Met Asn Met Thr Val Pro Cys Pro Thr Glu Gly Cys			
303	705 710 715			
305	agc ttg gag ctg ctc ttc caa cac ccg gtc caa gcc gac acc ctc acc	2901		
306	Ser Leu Glu Leu Leu Phe Gln His Pro Val Gln Ala Asp Thr Leu Thr			
307	720 725 730			
309	ctg tgg gtc act tcc ttc ttc atg gag tcc tcg cag gtc ctc ttt gac	2949		
310	Leu Trp Val Thr Ser Phe Phe Met Glu Ser Ser Gln Val Leu Phe Asp			
311	735 740 745 750			
313	aca gag atc ttg ctg gaa aac aag gag tca gtg cac ctg ggc ccc tta	2997		
314	Thr Glu Ile Leu Leu Glu Asn Lys Glu Ser Val His Leu Gly Pro Leu			
315	755 760 765			
317	gac act ttc tgt gac atc cca ctc acc atc aaa ctg cac gtg gat ggg	3045		
318	Asp Thr Phe Cys Asp Ile Pro Leu Thr Ile Lys Leu His Val Asp Gly			
319	770 775 780			
321	aag gtg tcg ggg gtg aaa gtc tac acc ttt gat gag agg ata gag att	3093		
322	Lys Val Ser Gly Val Lys Val Tyr Thr Phe Asp Glu Arg Ile Glu Ile			
323	785 790 795			
325	gat gca gca ctc ctg act tct cag ccc cac agt ccc ttg tgc tct ggc	3141		
326	Asp Ala Ala Leu Leu Thr Ser Gln Pro His Ser Pro Leu Cys Ser Gly			
327	800 805 810			

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:1425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24